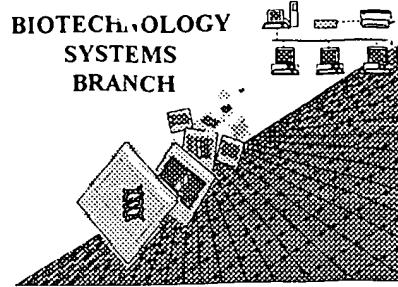


*Filing*

## RAW SEQUENCE LISTING ERROR REPORT



11/17/01?

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/435,770

RECEIVED

Source: 1652

FEB 02 2001

Date Processed by STIC: 1/24/2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/435,970</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input checked="" type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies primarily to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: <b>(2) INFORMATION FOR SEQ ID NO:X:</b> <b>(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")</b> <b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b> <b>This sequence is intentionally skipped</b>  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <b>&lt;210&gt; sequence id number</b> <b>&lt;400&gt; sequence id number</b> <b>000</b>	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

1652

*C:\V\tonada*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001  
TIME: 14:32:13

Input Set : A:\Yamamtol.app  
Output Set: N:\CRF3\01242001\I435770.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: YAMAMOTO, Takuo  
5 MARUTA, Kazuhiko  
6 KUBOTA, Michio  
7 FUKUDA, Shigeharu  
8 MIYAKE, Toshio  
10 <120> TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,  
11 TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING  
12 SACCHARIDES USING THE ENZYMES  
14 <130> FILE REFERENCE: YAMAMOTO=16A  
16 <140> CURRENT APPLICATION NUMBER: 09/435,770  
17 <141> CURRENT FILING DATE: 1999-11-08  
19 <150> PRIOR APPLICATION NUMBER: JP 258,394/1998  
20 <151> PRIOR FILING DATE: 1998-09-11  
22 <150> PRIOR APPLICATION NUMBER: JP 352,252/1998  
23 <151> PRIOR FILING DATE: 1998-12-11  
25 <150> PRIOR APPLICATION NUMBER: JP 16,931/1999  
26 <151> PRIOR FILING DATE: 1999-01-26  
28 <160> NUMBER OF SEQ ID NOS: 39  
30 <170> SOFTWARE: PatentIn Ver. 2.1

*ppr 1-15*  
**RECEIVED**

FEB 02 2001

TECH CENTER 1600/2900

#### ERRORRED SEQUENCES

241 <210> SEQ ID NO: 7  
242 <211> LENGTH: 2268  
243 <212> TYPE: DNA  
244 <213> ORGANISM: ARTHROBACTER sp.S34  
246 <400> SEQUENCE: 7  
E--> 247 cccgccagta cctaccgcct tcagatctcg gcggagttca ccctcttcga cgcggcgcgc  
248 60 ← → 60  
E--> 249 atcgtgcctt acctgcacccg cctcgccgc gactggctgt acctctcgcc gctgctcgag  
250 120 ← → 120  
E--> 251 tccgagtcgg gtcctcgca cggctacgac gtggtcgacc actcccgctt cgacgccc  
252 180  
E--> 253 cgcggcgggc cggaggggct cggcggacgtc tcccgtgcgg cgcacgagcg cggcatgggc  
254 240  
E--> 255 gtcgtcgctcg acatcggtcc caaccacgtc ggcgtcgccg cggcggacggc gaaccgctgg  
256 300  
E--> 257 tgggtggacg ttctggcccg tggacagcg ggactgtacg ccgactactt cgacatcgac  
258 360  
E--> 259 tgggagttcg gcggcggcag gctgcgcctg cccgtgtcg ggcacggccc cggcggacgtc  
260 420  
E--> 261 gacgcgtcga gagtggatgg cggcggacgtc gtctactacg agcaccgtt cccgtcgcc  
262 480  
E--> 263 gagggcaccg gcggcggcac cccgcgcgag gtgcacgacc ggcagcacta cggactgtatg  
264 540  
E--> 265 tcgtggcggc gggccgacca cggcgtcgccgt tccgcgtt gaaacacgtc

(see  
item 1 on  
Error Summary  
sheet)

*global  
format error*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001  
TIME: 14:32:13

Input Set : A:\Yamamtol.app  
Output Set: N:\CRF3\01242001\I435770.raw

266 600  
E--> 267 gccgcgtac gcgtcgaaga cccgcgcgtg ttgcacgaca cccaccgcga gatggccgc  
268 660  
E--> 269 tggatcgccg agggcctcg cgacggcctg cggtcgacc accccgacgg gtcgcgc  
270 720  
E--> 271 cccggcact acctgcgccg tctcgccgag ctgcggcaag gcaggccat ctgggtcgag  
272 780  
E--> 273 aagatcatcg agggcgacga gcggatgccc ccgcagtggc ccatacgccgg caccaccggc  
274 840  
E--> 275 tacgacgcgc tggccggat cgaccgggtg ctgcgtcgacc ccgcgggcga gcatccgc  
276 900  
E--> 277 acccagatcg tcgacgaggc ggcaggcagc cccggcgct gggccgagct gttcccgag  
278 960  
E--> 279 cgcaaggcgg ccgtcgcccg cggcatcctg aactccgaga tccgcccgt cgcccgaa  
280 1020  
E--> 281 ctggagagg tcgccccgcga cgtcgaagac ggcgtcgatcg agatcgccgc cgccctgtcc  
282 1080  
E--> 283 gtctaccgca gtcacctgcc gttcgggcgc gggcacctcg acgaagccgt ggccgc  
284 1140  
E--> 285 caggcccgag ccccccagct cgaggccgac ctgcggcccg tcggcgcagc gtcgccc  
286 1200  
E--> 287 ccggcaacc ccgcgcgct ccgttccag cagaccagcg gcatgatcat ggccaaggc  
288 1260  
E--> 289 gtcgaggaca acgcgttcta ccgttacccc cggctcacct cgctgaccga ggtcgggg  
290 1320  
E--> 291 gaccgcgagcc tttcgcatcgat cgacgcggcc gccttccacg cggcgcagcg cgaccgc  
292 1380  
E--> 293 gcccggctgc ctagtgcgtat gacgacgcgtg accacccacg acaccaagcg cagcgaagac  
294 1440  
E--> 295 acccgggcgc ggttccatcg cgtcgccgag gcggccgaaac gtcggccgcg cttcc  
296 1500  
E--> 297 gaggtcgccg ggctcatcg aacggccgac cgggtgtgg agaacatgtat ctggcaggcg  
298 1560  
E--> 299 atcgtcgccg cgtggccggc gagccggag cggctcgagg cttacgcgt gaaggccgc  
300 1620  
E--> 301 cgcgaagccg cgcgtcgac cgactggatc gacggcgacc ccgcgttca agagcggctg  
302 1680  
E--> 303 acccgccctgg tcacggtcgc cgtcgaggag ccgtcgatcg acgagctgt cgagcgg  
304 1740  
E--> 305 gtcgacgagc tgacggccgc cgggtactcc aacggccctcg cggcgaagct gtcgac  
306 1800  
E--> 307 ctcgcggccg gaaccccgaa cgtgtaccag ggcacggaac gtcggaccg gtcgtgg  
308 1860  
E--> 309 gacccggaca accgtcgccc cgtggatttc gccgcggcat ccgagctgt cgaccgc  
310 1920  
E--> 311 gacggccgc ggcggccgc cgtcgacgag accggcgccg tcaagacgct cgtcgat  
312 1980  
E--> 313 cgcgcgtgc ggctgcgccg cgaccggccc gagctgttca ccgcgttca cccggtc  
314 2040

*mane  
even*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001  
TIME: 14:32:13

Input Set : A:\Yamamtol.app  
Output Set: N:\CRF3\01242001\I435770.raw

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FEB 02 2001

E--> 315 gcgcgcggcg cgaggccga gcacctgatc ggcttcgacc gcggcggcgc gatcgccctg  
316 2100  
E--> 317 gccacccggcc tgccgctcggt cctcgccgccc gcaggcggct gggggcacac ggtcgctcgac  
318 2160  
E--> 319 gtcggcgagc ggagcctgatc cgacgagctg accggccgatc agggccgcgg agcggcgcgc  
320 2220  
E--> 321 gtggccgagt ttttgcggat ctacccgtc gcccgtctgg tggagaca  
322 2268  
325 <210> SEQ ID NO: 8  
326 <211> LENGTH: 28  
327 <212> TYPE: DNA  
328 <213> ORGANISM: ARTHROBACTER sp.S34  
330 <400> SEQUENCE: 8  
E--> 331 ttttttaata aaatcaggag gaaaaaat  
332 28  
529 <210> SEQ ID NO: 17  
530 <211> LENGTH: 1725  
531 <212> TYPE: DNA  
532 <213> ORGANISM: ARTHROBACTER sp.S34  
534 <400> SEQUENCE: 17  
E--> 535 atgaaccgac gattcccggt ctggcgcccc caggccgcgc aggtgacgct cgtcggtggc  
536 60  
E--> 537 caaggccgcg ccgaactccc gctgaccgcg gacgagaacg gatggtgggc tcttcagcag  
538 120  
E--> 539 ccgtggacg gcccggcccgatc cctcgatcgac tacggctacc tcgtcgacgg caagggcccc  
540 180  
E--> 541 ttccggacc cgggtcgatc gcccggcccg cggccgtgc acgagctcggtt cccgaaattc  
542 240  
E--> 543 gacccggcccgatc gtttgcgtg gggcgacgac ggtatggcgcg gccgagacccatc  
544 300  
E--> 545 gtatctacg aactgcacgt cggcacccatc accccctgagg gaacgctggatc cagcgccatc  
546 360  
E--> 547 cgtcgctcg accacccgtt gcccgtcgatc gtcgacgcgg tcgagctgtt gcccgtcaac  
548 420  
E--> 549 gcttcaacg gcacccacgg ctggggctac gacggggatc tctggatcgc ggtgcacgag  
550 480  
E--> 551 ccctacggcg gcccggaggc gtaccagcgatc ttcgtcgatc cctggccacgc cccggccctc  
552 540  
E--> 553 gccgtcgatc aggacgtcgatc ctacaaccatc ctggggcccgatc gcccggccatc  
554 600  
E--> 555 ttccggccctt acctcggtt gggcgccgcg aacacccgtt gtcgacgcgtt gacccgtcgatc  
556 660  
E--> 557 gggccgtctt ccgtcgatc gtcgacgcgtt atcatcgatc acgacgtgtt ctggctcgatc  
558 720  
E--> 559 gacatgcacg ccgtcgatc gtcgacgcgtt gtcgacgcgtt gtcgacgcgtt cccggcccgatc  
560 780  
E--> 561 ctgcacccgtt tcgtcgatc gtcgacgcgtt gtcgacgcgtt gtcgacgcgtt cccggcccgatc  
562 840  
E--> 563 ccgtcgatc tcgtcgatc gtcgacgcgtt gtcgacgcgtt gtcgacgcgtt cccggcccgatc  
*same*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001  
TIME: 14:32:13

Input Set : A:\Yamamtol.app  
Output Set: N:\CRF3\01242001\I435770.raw

564 900  
E--> 565 ggcacggct acggcctcgaa cccccagtgg gacgacgacg tgcaccacgc ggtgcacgcc  
566 960  
E--> 567 aacgtgaccg gcgagaccgt cggtactaac gccgacttcg gcgggctcg ggccctcg  
568 1020  
E--> 569 aagggtttcc agcgccgctg gttccacgac ggcacctggt cgagcttccg cgagcggcac  
570 1080  
E--> 571 cacggccggc cgctcgaccc cgacatccc ttccggccggc tcgtcgccctt cgccgaggat  
572 1140  
E--> 573 cacgaccagg tcggcaaccg agcggtcgcc gaccgcattt cggcgcaggat cggcgagggt  
574 1200  
E--> 575 tcgctcgccg ccgcggccggc gtcgtgtcg ctccggccgt tcaccccat gctgttcatg  
576 1260  
E--> 577 ggcgaggagt ggggcgcgcg caccgggtgg cagttttca cttccaccc cgagcccgag  
578 1320  
E--> 579 ctgggggagg cgacggcgcg cgggcgcattt gccgagttcg cccgcattggg ctgggacccg  
580 1380  
E--> 581 gcagtcgtgc ccgacccgca ggacccggcc accttcgccc gtcgcaccc gactggtcc  
582 1440  
E--> 583 gagcccgagc gggAACCGCA cgcgggcctg ctcgccttctt acaccgaccc gatcgccgt  
584 1500  
E--> 585 cggcgcgagc tgccggtcga tgcgcggcg cggcagggtgg atgcgcacga ggcgcgcggc  
586 1560  
E--> 587 gtcttcgcgt tcagccgcgg cccgctgcgg gtcacggtcg cgctgcgcggcc cggaccggtc  
588 1620  
E--> 589 ggggtgcccgg acacggggg cctcgtgtc gcctacggcg aggtgcgcgc cggcgccggc  
590 1680  
E--> 591 ggactgcacc tcgacggggcc gggagccgcg atcgtgcgcgc tcgag  
592 1725  
595 <210> SEQ ID NO: 18  
596 <211> LENGTH: 23  
597 <212> TYPE: DNA  
598 <213> ORGANISM: ARTHROBACTER sp.S34  
600 <400> SEQUENCE: 18  
E--> 601 gcsaaccgst ggtggggca cgt  
602 23  
605 <210> SEQ ID NO: 19  
606 <211> LENGTH: 3252  
607 <212> TYPE: DNA  
608 <213> ORGANISM: ARTHROBACTER sp.S34  
610 <220> FEATURE:  
611 <221> NAME/KEY: 5'UTR  
612 <222> LOCATION: (1)..(742)  
614 <220> FEATURE:  
615 <221> NAME/KEY: CDS  
616 <222> LOCATION: (743)..(3013)  
618 <220> FEATURE:  
619 <221> NAME/KEY: 3'UTR  
620 <222> LOCATION: (742)..(3014)



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001  
TIME: 14:32:13

Input Set : A:\Yamamtol.app  
Output Set: N:\CRF3\01242001\I435770.raw

622 <400> SEQUENCE: 19  
E--> 623 atgccgacga cgaactttag cgctttctcg ggcacccgag agagcggtcc ggcacggcg  
624 60  
E--> 626 gcccggctgt ccacgacgag cacgatcgcg gcgagcgccg cgacgacggc gaccggcagg  
627 120  
E--> 629 cgcctgtat tgctggcgaa ggtgagcacg atgaagacca ctcgaggcc ctcgagcaac  
630 180  
E--> 632 acaccttga acgacacggt gaacgcgtac caatcgaga cccgaaccg gctctcgcc  
633 240  
E--> 635 cggcgctct cggccgcctc gacctgacgc cgaaaggcag ctcctcgctc acggagagcc  
636 300  
E--> 638 ctgcgcctg cgcgcgcag caccgcctg cgccagccagc cgagccgaa gacgagcagc  
639 360  
E--> 641 aacccggcga cgacgaggcg cagcacggcc agcggcagca gcaggatcgc gggaccgacg  
642 420  
E--> 644 agcgcgacgg cgcggccag caccaccacg ggcacggcg cacctgtcag cgccgaccgc  
645 480  
E--> 647 cagctgcggg tggcgccac cgacgacgacg atcgtggtcg ctcaccgc ctcgaccacg  
648 540  
E--> 650 caggcgagga acacggcggc gaacagggcg acggcggtca tcggcccgac agacggttga  
651 600  
E--> 653 ccatcaeggc acgctagcgc cattgtcac aggaagggcc aagacgccccg caacgcggca  
654 660  
E--> 656 cccgtggacg ggcgttaccg ggcgtgtacc gatcgtgtca accggtggcg cccgccccga  
657 720  
E--> 659 gcacctgcgt agattcgcc tc gtg ccc gcc agt acc tac cgc ctt cag atc  
660 772  
661 Met Pro Ala Ser Thr Tyr Arg Leu Gln Ile  
662 1 5 10  
E--> 664 tcg gcg gag ttc acc ctc ttc gac gcg gcg cgc atc gtg ccc tac ctg  
665 820  
666 Ser Ala Glu Phe Thr Leu Phe Asp Ala Ala Arg Ile Val Pro Tyr Leu  
667 15 20 25  
E--> 669 cac cgc ctc ggc gcc gac tgg ctg tac ctc tcc ccg ctg ctc gag tcc  
670 868  
671 His Arg Leu Gly Ala Asp Trp Leu Tyr Leu Ser Pro Leu Leu Glu Ser  
672 30 35 40  
E--> 674 gag tcg ggc tcc tcg cac ggc tac gac gtg gtc gac cac tcc cgc gtc  
675 916  
676 Glu Ser Gly Ser Ser His Gly Tyr Asp Val Val Asp His Ser Arg Val  
677 45 50 55  
E--> 679 gac gcc gcc cgc ggc ggg ccg gag ggg ctc gcc gag ctc tcc cgt gcg  
680 964  
681 Asp Ala Ala Arg Gly Pro Glu Gly Leu Ala Glu Leu Ser Arg Ala  
682 60 65 70  
E--> 684 gcg cac gag cgc ggc atg ggc gtc gtc gtc gac atc gtg ccc aac cac  
685 1012  
686 Ala His Glu Arg Gly Met Gly Val Val Asp Ile Val Pro Asn His  
687 75 80 85 90



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001  
TIME: 14:32:13

Input Set : A:\Yamamto1.app  
Output Set: N:\CRF3\01242001\I435770.raw

E--> 689 gtc ggc gtc gcg acg ccg aag gcg aac cgc tgg tgg tgg gac gtt ctg  
 690 1060  
 691 Val Gly Val Ala Thr Pro Lys Ala Asn Arg Trp Trp Trp Asp Val Leu  
 692 95 100 105  
 E--> 694 gcc cgt gga cag cgg tcg gag tac gcc gac tac ttc gac atc gac tgg  
 695 1108  
 696 Ala Arg Gly Gln Arg Ser Glu Tyr Ala Asp Tyr Phe Asp Ile Asp Trp  
 697 110 115 120  
 E--> 699 gag ttc ggc ggc agg ctg cgc ctg ccc gtg ctc ggc gac ggc ccc  
 700 1156  
 701 Glu Phe Gly Gly Arg Leu Arg Leu Pro Val Leu Gly Asp Gly Pro  
 702 125 130 135  
 E--> 704 gac gag ctc gac gcg ctg aga gtg gat ggc gac gag ctc gtc tac tac  
 705 1204  
 706 Asp Glu Leu Asp Ala Leu Arg Val Asp Gly Asp Glu Leu Val Tyr Tyr  
 707 140 145 150  
 E--> 709 gag cac cgc ttc ccg atc gcc gag ggc acc ggc ggc acc ccc cgc  
 710 1252  
 711 Glu His Arg Phe Pro Ile Ala Glu Gly Thr Gly Gly Thr Pro Arg  
 712 155 160 165 170  
 E--> 714 gag gtg cac gac cgg cag cac tac gag ctg atg tcg tgg cgg cgg gcc  
 715 1300  
 716 Glu Val His Asp Arg Gln His Tyr Glu Leu Met Ser Trp Arg Arg Ala  
 717 175 180 185  
 E--> 719 gac cac gac ctc aac tac cgc cgc ttc ttc gcc gtg aac acg ctc gcc  
 720 1348  
 721 Asp His Asp Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala  
 722 190 195 200  
 E--> 724 gcc gta cgc gtc gaa gac ccg cgc gtg ttc gac gac acc cac cgc gag  
 725 1396  
 726 Ala Val Arg Val Glu Asp Pro Arg Val Phe Asp Asp Thr His Arg Glu  
 727 205 210 215  
 E--> 729 atc ggc cgc tgg atc gcc gag ggc ctc gtc gac ggc ctg cgc gtc gac  
 730 1444  
 731 Ile Gly Arg Trp Ile Ala Glu Gly Leu Val Asp Gly Leu Arg Val Asp  
 732 220 225 230  
 E--> 734 cac ccc gac ggg ctg cgc gcc ccc ggc gac tac ctg cgc cgt ctc gcc  
 735 1492  
 736 His Pro Asp Gly Leu Arg Ala Pro Gly Asp Tyr Leu Arg Arg Leu Ala  
 737 235 240 245 250  
 E--> 739 gag ctc gcc caa ggc agg ccg atc tgg gtc gag aag atc atc gag ggc  
 740 1540  
 741 Glu Leu Ala Gln Gly Arg Pro Ile Trp Val Glu Lys Ile Ile Glu Gly  
 742 255 260 265  
 E--> 744 gac gag cgg atg ccc ccg cag tgg ccc atc gcc ggc acc acc ggc tac  
 745 1588  
 746 Asp Glu Arg Met Pro Pro Gln Trp Pro Ile Ala Gly Thr Thr Gly Tyr  
 747 270 275 280  
 E--> 749 gac gcg ctg gcc ggg atc gac cgg gtg ctc gtc gac ccc gcg ggc gag

*Same*

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Input Set : A:\Yamamtol.app  
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750 1636  
 751 Asp Ala Leu Ala Gly Ile Asp Arg Val Leu Val Asp Pro Ala Gly Glu  
 752 285 290 295  
 E--> 754 cat ccg ctc acc cag atc gtc gac gag gcg gca ggc agc ccc cgg cgc  
 755 1684  
 756 His Pro Leu Thr Gln Ile Val Asp Glu Ala Ala Gly Ser Pro Arg Arg  
 757 300 305 310  
 E--> 759 tgg gcc gag ctg gtt ccc gag cgc aag cgg gcc gtc gcc cgc ggc atc  
 760 1732  
 761 Trp Ala Glu Leu Val Pro Glu Arg Lys Arg Ala Val Ala Arg Gly Ile  
 762 315 320 325 330  
 E--> 764 ctg aac tcc gag atc cgc cgc gtc gcc cgc gaa ctc gga gag gtc gcc  
 765 1780  
 766 Leu Asn Ser Glu Ile Arg Arg Val Ala Arg Glu Leu Gly Glu Val Ala  
 767 335 340 345  
 E--> 769 ggc gac gtc gaa gac gcg ctc gtc gag atc gcc gcc gcc ctg tcc gtc  
 770 1828  
 771 Gly Asp Val Glu Asp Ala Leu Val Glu Ile Ala Ala Ala Leu Ser Val  
 772 350 355 360  
 E--> 774 tac cgc agc tac ctg ccg ttc ggg cgc gag cac ctc gac gaa gcc gtg  
 775 1876  
 776 Tyr Arg Ser Tyr Leu Pro Phe Gly Arg Glu His Leu Asp Glu Ala Val  
 777 365 370 375  
 E--> 779 gcc gcc gcg cag gcc gca gcc ccc cag ctc gag gcc gac ctc gcc gcc  
 780 1924  
 781 Ala Ala Ala Gln Ala Ala Ala Pro Gln Leu Glu Ala Asp Leu Ala Ala  
 782 380 385 390  
 E--> 784 gtc ggc gca gcg ctc gcc gac ccg ggc aac ccc gcc gcg ctc cgc ttc  
 785 1972  
 786 Val Gly Ala Ala Leu Ala Asp Pro Gly Asn Pro Ala Ala Leu Arg Phe  
 787 395 400 405 410  
 E--> 789 cag cag acc agc ggc atg atc atg gcc aag ggc gtc gag gac aac gcg  
 790 2020  
 791 Gln Gln Thr Ser Gly Met Ile Met Ala Lys Gly Val Glu Asp Asn Ala  
 792 415 420 425  
 E--> 794 ttc tac cgc tac ccc ccg ctc acc tcg ctg acc gag gtc ggg gga gac  
 795 2068  
 796 Phe Tyr Arg Tyr Pro Arg Leu Thr Ser Leu Thr Glu Val Gly Gly Asp  
 797 430 435 440  
 E--> 799 ccg agc ctg ttc gcg atc gac gcg gcc ttc cac gcg gcg cag cgc  
 800 2116  
 801 Pro Ser Leu Phe Ala Ile Asp Ala Ala Ala Phe His Ala Ala Gln Arg  
 802 445 450 455  
 E--> 804 gac cgc gcc gcc ccg ctg ccc gag tcg atg acg acg ctg acc acc cac  
 805 2164  
 806 Asp Arg Ala Ala Arg Leu Pro Glu Ser Met Thr Thr Leu Thr Thr His  
 807 460 465 470  
 E--> 809 gac acc aag cgc agc gaa gac acc ccg gcg cgg atc acc gcg ctc gcc  
 810 2212

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Input Set : A:\Yamamtol.app  
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811 Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Thr Ala Leu Ala  
 812 475 480 485 490  
 E--> 814 gag gcc ccc gaa cgc tgg cgg cgc ttc ctg acc gag gtc ggc ggg ctc  
 815 2260  
 816 Glu Ala Pro Glu Arg Trp Arg Arg Phe Leu Thr Glu Val Gly Gly Leu  
 817 495 500 505  
 E--> 819 atc gga acg ggc gac cgg gtg ctg gag aac ctg atc tgg cag gcg atc  
 820 2308  
 821 Ile Gly Thr Gly Asp Arg Val Leu Glu Asn Leu Ile Trp Gln Ala Ile  
 822 510 515 520  
 E--> 824 gtc ggc gcg tgg ccg cgc agc cgg gag cgg ctc gag gcc tac gcg ctg  
 825 2356  
 826 Val Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Glu Ala Tyr Ala Leu  
 827 525 530 535  
 E--> 829 aag gcc gcg cgc gaa gcc ggc gag tcg acc gac tgg atc gac ggc gac  
 830 2404  
 831 Lys Ala Ala Arg Glu Ala Gly Glu Ser Thr Asp Trp Ile Asp Gly Asp  
 832 540 545 550  
 E--> 834 ccc gcg ttc gaa gag cgg ctg acc cgc ctg gtc acg gtc gcc gtc gag  
 835 2452  
 836 Pro Ala Phe Glu Glu Arg Leu Thr Arg Leu Val Thr Val Ala Val Glu  
 837 555 560 565 570  
 E--> 839 gag ccg ctc gtg cac gag ctg ctc gag cgg ctc gtc gac gag ctg acg  
 840 2500  
 841 Glu Pro Leu Val His Glu Leu Leu Glu Arg Leu Val Asp Glu Leu Thr  
 842 575 580 585  
 E--> 844 gcg gcc ggg tac tcc aac ggc ctc gcg gcg aag ctg ctg cag ctg ctc  
 845 2548  
 846 Ala Ala Gly Tyr Ser Asn Gly Leu Ala Ala Lys Leu Leu Gln Leu Leu  
 847 590 595 600  
 E--> 849 gcc ccc gga acc ccc gac gtg tac cag ggc acg gaa cgc tgg gac cgg  
 850 2596  
 851 Ala Pro Gly Thr Pro Asp Val Tyr Gln Gly Thr Glu Arg Trp Asp Arg  
 852 605 610 615  
 E--> 854 tcg ctg gtg gac ccg gac aac cgt cgc ccc gtg gat ttc gcc gcg gca  
 855 2644  
 856 Ser Leu Val Asp Pro Asp Asn Arg Arg Pro Val Asp Phe Ala Ala Ala  
 857 620 625 630  
 E--> 859 tcc gag ctg ctc gac cgc ctc gac ggc ggc tgg cgg ccc gtc gac  
 860 2692  
 861 Ser Glu Leu Leu Asp Arg Leu Asp Gly Gly Trp Arg Pro Pro Val Asp  
 862 635 640 645 650  
 E--> 864 gag acc ggc gcg gtc aag acg ctc gtc gtc tcc cgc gcg ctg cgg ctg  
 865 2740  
 866 Glu Thr Gly Ala Val Lys Thr Leu Val Val Ser Arg Ala Leu Arg Leu  
 867 655 660 665  
 E--> 869 cgc cgc gac cgg ccc gag ctg ttc acc gcg tac cac ccg gtc acg gcg  
 870 2788  
 871 Arg Arg Asp Arg Pro Glu Leu Phe Thr Ala Tyr His Pro Val Thr Ala



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Input Set : A:\Yamamtol.app  
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872               670               675               680  
E--> 874 cgc ggc gcg cag gcc gag cac ctg atc ggc ttc gac cgc ggc ggc gcg  
875 2836  
876 Arg Gly Ala Gln Ala Glu His Leu Ile Gly Phe Asp Arg Gly Gly Ala  
877         685               690               695  
E--> 879 atc gcc ctg gcc acc cgc ctg ccg ctc ggc ctc gcc gcc gca ggc ggc  
880 2884  
881 Ile Ala Leu Ala Thr Arg Leu Pro Leu Gly Leu Ala Ala Gly Gly  
882         700               705               710  
E--> 884 tgg ggc gac acg gtc gtc gac gtc ggc gag cgg agc ctg cgc gac gag  
885 2932  
886 Trp Gly Asp Thr Val Val Asp Val Gly Glu Arg Ser Leu Arg Asp Glu  
887 715               720               725               730  
E--> 889 ctg acc ggc cgc gag gcc cgc gga gcg gcg cgc gtg gcc gag ttg ttc  
890 2980  
891 Leu Thr Gly Arg Glu Ala Arg Gly Ala Ala Arg Val Ala Glu Leu Phe  
892         735               740               745  
E--> 894 gcc gac tac ccc gtc gcc ctg ctg gtg gag aca tgaaccgacg attcccggtc  
895 3033  
896 Ala Asp Tyr Pro Val Ala Leu Leu Val Glu Thr  
897         750               755  
E--> 899 tggcgcccc aggccgcgca ggtgacgctc gtcgtgggcc aaggccgcgc cgaactcccg  
900 3093  
E--> 902 ctgaccgcg acgagaacgg atggtgggct cttcagcagc cgtggacgg cggcccccac  
903 3153  
E--> 905 ctcgtcgact acggctacct cgtcgacggc aaggcccct tcgccgaccc gcggtcgctg  
906 3213  
E--> 908 cggcagccgc gcggcgtgca cgagctcggc cgcgaattc  
909 3252  
913 <210> SEQ ID NO: 20  
914 <211> LENGTH: 26  
915 <212> TYPE: DNA  
916 <213> ORGANISM: Artificial Sequence  
918 <220> FEATURE:  
919 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
921 <400> SEQUENCE: 20  
E--> 922 atgcccggcca gtacacctaccg cttca  
923 26  
926 <210> SEQ ID NO: 21  
927 <211> LENGTH: 25  
928 <212> TYPE: DNA  
929 <213> ORGANISM: Artificial Sequence  
931 <220> FEATURE:  
932 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
934 <400> SEQUENCE: 21  
E--> 935 tcatgtctcc accagcaggg cgacg  
936 25  
939 <210> SEQ ID NO: 22  
940 <211> LENGTH: 50

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941 <212> TYPE: DNA  
942 <213> ORGANISM: Artificial Sequence  
944 <220> FEATURE:  
945 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
947 <400> SEQUENCE: 22  
**E--> 948 aattctttt taataaaatc aggaggaatc tagatgttta ctagtctgca**  
949 50  
952 <210> SEQ ID NO: 23  
953 <211> LENGTH: 42  
954 <212> TYPE: DNA  
955 <213> ORGANISM: Artificial Sequence  
957 <220> FEATURE:  
958 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
960 <400> SEQUENCE: 23  
**E--> 961 gacttagaaa catctagatt ctccttgatt ttattaaaaa ag**  
962 42  
965 <210> SEQ ID NO: 24  
966 <211> LENGTH: 33  
967 <212> TYPE: DNA  
968 <213> ORGANISM: Artificial Sequence  
970 <220> FEATURE:  
971 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
973 <400> SEQUENCE: 24  
**E--> 974 aaatctagat gccccccagt acctaccgcc ttc**  
975 33  
978 <210> SEQ ID NO: 25  
979 <211> LENGTH: 33  
980 <212> TYPE: DNA  
981 <213> ORGANISM: Artificial Sequence  
983 <220> FEATURE:  
984 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
986 <400> SEQUENCE: 25  
**E--> 987 aaaactagtt tatcatgtct ccaccagcac ggc**  
988 33  
991 <210> SEQ ID NO: 26  
992 <211> LENGTH: 22  
993 <212> TYPE: DNA  
994 <213> ORGANISM: Artificial Sequence  
996 <220> FEATURE:  
997 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
999 <400> SEQUENCE: 26  
**E--> 1000 atcgggtgatg tcggcgatat ag**  
1001 22  
1004 <210> SEQ ID NO: 27  
1005 <211> LENGTH: 29  
1006 <212> TYPE: DNA  
1007 <213> ORGANISM: Artificial Sequence  
1009 <220> FEATURE:  
1010 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC

*None*

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Input Set : A:\Yamamtol.app  
Output Set: N:\CRF3\01242001\I435770.raw

1012 <400> SEQUENCE: 27  
E--> 1013 gtactggcgg gcatatttt tcctcctga  
1014 29  
1017 <210> SEQ ID NO: 28  
1018 <211> LENGTH: 31  
1019 <212> TYPE: DNA  
1020 <213> ORGANISM: Artificial Sequence  
1022 <220> FEATURE:  
1023 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
1025 <400> SEQUENCE: 28  
E--> 1026 aatcaggagg aaaaaatatg cccgccagta c  
1027 31  
1030 <210> SEQ ID NO: 29  
1031 <211> LENGTH: 22  
1032 <212> TYPE: DNA  
1033 <213> ORGANISM: Artificial Sequence  
1035 <220> FEATURE:  
1036 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
1038 <400> SEQUENCE: 29  
E--> 1039 tcgacgatct gggtgagcgg at  
1040 22  
1043 <210> SEQ ID NO: 30  
1044 <211> LENGTH: 22  
1045 <212> TYPE: DNA  
1046 <213> ORGANISM: Artificial Sequence  
1048 <220> FEATURE:  
1049 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
1051 <400> SEQUENCE: 30  
E--> 1052 tcgacgagca cccggatcgat cc  
1053 22  
1056 <210> SEQ ID NO: 31  
1057 <211> LENGTH: 26  
1058 <212> TYPE: DNA  
1059 <213> ORGANISM: Artificial Sequence  
1061 <220> FEATURE:  
1062 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
1064 <400> SEQUENCE: 31  
E--> 1065 cartgggayg aygaygttca ycaygc *(see item 10 on Error Summary Sheet)*  
1066 26  
1069 <210> SEQ ID NO: 32  
1070 <211> LENGTH: 2218  
1071 <212> TYPE: DNA  
1072 <213> ORGANISM: Artificial Sequence  
1074 <220> FEATURE:  
1075 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
1077 <220> FEATURE:  
1078 <221> NAME/KEY: CDS  
1079 <222> LOCATION: (477)...(2201)  
1081 <220> FEATURE:

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Input Set : A:\Yamamtol.app  
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1082 <221> NAME/KEY: 3'UTR  
 1083 <222> LOCATION: (2202)..(2218)  
 E--> 1085 <400> SEQUENCE: 33  
 E--> 1086 ctgcagctgc tcgccccgg aaccccccac gtgtaccagg gcacggAACG ctgggaccgg  
 1087 60  
 E--> 1089 tcgcttgtgg acccggacaa ccgtcgcccc gtggatttcg ccgcggcatc cgagctgctc  
 1090 120  
 E--> 1092 gaccgcctcg acggcggctg gcggccgccc gtcgacgaga ccggcgcggt caagacgctc  
 1093 180  
 E--> 1095 gtcgtctccc gcgcgctgcg gctgcgcgcg accggcccg agctgttac cgcgtaccac  
 1096 240  
 E--> 1098 ccgggtcacgg cgcgccgcg gcaggccgag cacctgatcg gcttcgaccg cggcggccgc  
 1099 300  
 E--> 1101 atcgccctgg ccacccgcct gccgctcgcc ctcgcccgg caggcggctg gggcgacacg  
 1102 360  
 E--> 1104 gtcgtcgacg tcggcgagcg gagcctgcgc gacgagctga ccggccgcga ggcccgcgga  
 1105 420  
 E--> 1107 gcgccgcg tggccgagtt gttcgccgac taccggctcg ccctgcttgt ggagac atg  
 1108 479  
 1109 Met  
 1110 1  
 E--> 1112 aac cga cga ttc ccg gtc tgg gcg ccc cag gcc gcg cag gtg acg ctc  
 1113 527  
 1114 Asn Arg Arg Phe Pro Val Trp Ala Pro Gln Ala Ala Gln Val Thr Leu  
 1115 5 10 15  
 E--> 1117 gtc gtg ggc caa ggc cgc gcc gaa ctc ccg ctg acc cgc gac gag aac  
 1118 575  
 1119 Val Val Gly Gln Gly Arg Ala Glu Leu Pro Leu Thr Arg Asp Glu Asn  
 1120 20 25 30  
 E--> 1122 gga tgg tgg gct ctt cag cag ccg tgg gac ggc ggc ccc gac ctc gtc  
 1123 623  
 1124 Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu Val  
 1125 35 40 45  
 E--> 1127 gac tac ggc tac ctc gtc gac ggc aag ggc ccc ttc gcc gac ccg cgg  
 1128 671  
 1129 Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro Arg  
 1130 50 55 60 65  
 E--> 1132 tcg ctg cgg cag ccg cgc ggc gtg cac gag ctc ggc cgc gaa ttc gac  
 1133 719  
 1134 Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe Asp  
 1135 70 75 80  
 E--> 1137 ccc gcc cgc tac gcg tgg ggc gac gac gga tgg cgc ggc cga gac ctc  
 1138 767  
 1139 Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp Leu  
 1140 85 90 95  
 E--> 1142 acc gga gcc gtg atc tac gaa ctg cac gtc ggc acc ttc acc cct gag  
 1143 815  
 1144 Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro Glu  
 1145 100 105 110



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Input Set : A:\Yamamtol.app  
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E--> 1147 gga acg ctg gac agc gcc atc cgt cgc ctc gac cac ctg gtg cgc ctc  
 1148 863  
 1149 Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg Leu  
 1150 115 120 125  
 E--> 1152 ggc gtc gac gcg gtc gag ctg ctg ccc gtc aac gcg ttc aac ggc acc  
 1153 911  
 1154 Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly Thr  
 1155 130 135 140 145  
 E--> 1157 cac ggc tgg ggc tac gac ggg gtg ctc tgg tac gcg gtg cac gag ccc  
 1158 959  
 1159 His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu Pro  
 1160 150 155 160  
 E--> 1162 tac ggc ggc ccg gag gcg tac cag cgc ttc gtc gac gcc tgc cac gcc  
 1163 1007  
 1164 Tyr Gly Gly Pro Glu Ala Tyr Gln Arg Phe Val Asp Ala Cys His Ala  
 1165 165 170 175  
 E--> 1167 cgc ggc ctc gcc gtc gtg cag gac gtc gtc tac aac cac ctg ggc ccg  
 1168 1055  
 1169 Arg Gly Leu Ala Val Val Gln Asp Val Val Tyr Asn His Leu Gly Pro  
 1170 180 185 190  
 E--> 1172 agc ggc aac cac ctg ccc gac ttc ggc ccc tac ctc ggg tcg ggc gcc  
 1173 1103  
 1174 Ser Gly Asn His Leu Pro Asp Phe Gly Pro Tyr Leu Gly Ser Gly Ala  
 1175 195 200 205  
 E--> 1177 gcc aac acc tgg ggc gac gcg ctg aac ctc gac ggg ccg ctc tcc gac  
 1178 1151  
 1179 Ala Asn Thr Trp Gly Asp Ala Leu Asn Leu Asp Gly Pro Leu Ser Asp  
 1180 210 215 220 225  
 E--> 1182 gag gtg cgg cgg tac atc atc gac aac gcg gtg tac tgg ctg cgc gac  
 1183 1199  
 1184 Glu Val Arg Arg Tyr Ile Ile Asp Asn Ala Val Tyr Trp Leu Arg Asp  
 1185 230 235 240  
 E--> 1187 atg cac gcc gac ggg ctg cgg ctc gac gcc gtg cac gcg ctg cgc gac  
 1188 1247  
 1189 Met His Ala Asp Gly Leu Arg Leu Asp Ala Val His Ala Leu Arg Asp  
 1190 245 250 255  
 E--> 1192 gcc cgc gcg ctg cac ctg ctc gaa gag ctc gcc gcc gtc gac gag  
 1193 1295  
 1194 Ala Arg Ala Leu His Leu Leu Glu Glu Leu Ala Ala Arg Val Asp Glu  
 1195 260 265 270  
 E--> 1197 ctg gcg ggc gag ctc ggc cgg ccg ctg acg ctc atc gcc gag agc gac  
 1198 1343  
 1199 Leu Ala Gly Glu Leu Gly Arg Pro Leu Thr Leu Ile Ala Glu Ser Asp  
 1200 275 280 285  
 E--> 1202 ctg aac gac ccg aag ctg atc cgc tcc cgc gcg gac ggc tac ggc  
 1203 1391  
 1204 Leu Asn Asp Pro Lys Leu Ile Arg Ser Arg Ala Ala His Gly Tyr Gly  
 1205 290 295 300 305  
 E--> 1207 ctc gac gcc cag tgg gac gac gtg cac cac gcg gtg cac gcc aac

*Danne*

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Input Set : A:\Yamamtol.app  
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1208 1439  
 1209 Leu Asp Ala Gln Trp Asp Asp Asp Val His His Ala Val His Ala Asn  
 1210 310 315 320  
 E--> 1212 gtg acc ggc gag acc gtc ggc tac tac gcc gac ttc ggc ggg ctc ggc  
 1213 1487  
 1214 Val Thr Gly Glu Thr Val Gly Tyr Tyr Ala Asp Phe Gly Gly Leu Gly  
 1215 325 330 335  
 E--> 1217 gcc ctc gtc aag gtg ttc cag cgc ggc tgg ttc cac gac ggc acc tgg  
 1218 1535  
 1219 Ala Leu Val Lys Val Phe Gln Arg Gly Trp Phe His Asp Gly Thr Trp  
 1220 340 345 350  
 E--> 1222 tcg agc ttc cgc gag cgg cac cac ggc cgg ccg ctc gac ccc gac atc  
 1223 1583  
 1224 Ser Ser Phe Arg Glu Arg His His Gly Arg Pro Leu Asp Pro Asp Ile  
 1225 355 360 365  
 E--> 1227 ccg ttc cgc cgg ctc gtc gcc ttc gcg cag gat cac gac cag gtc ggc  
 1228 1631  
 1229 Pro Phe Arg Arg Leu Val Ala Phe Ala Gln Asp His Asp Gln Val Gly  
 1230 370 375 380 385  
 E--> 1232 aac cga gcg gtc ggc gac cgc atg tcg gcg cag gtc ggc gag ggt tcg  
 1233 1679  
 1234 Asn Arg Ala Val Gly Asp Arg Met Ser Ala Gln Val Gly Glu Gly Ser  
 1235 390 395 400  
 E--> 1237 ctc gcc gcc gcg gcg gcg ctc gtg ctg ctc ggc ccg ttc acc ccg atg  
 1238 1727  
 1239 Leu Ala Ala Ala Ala Leu Val Leu Leu Gly Pro Phe Thr Pro Met  
 1240 405 410 415  
 E--> 1242 ctg ttc atg ggc gag gag tgg ggc gcg cgc acc ccg tgg cag ttc ttc  
 1243 1775  
 1244 Leu Phe Met Gly Glu Glu Trp Gly Ala Arg Thr Pro Trp Gln Phe Phe  
 1245 420 425 430  
 E--> 1247 acc tcc cac ccc gag ccc gag ctg ggg gag gcg acg gcg cgc ggg cgc  
 1248 1823  
 1249 Thr Ser His Pro Glu Pro Glu Leu Gly Glu Ala Thr Ala Arg Gly Arg  
 1250 435 440 445  
 E--> 1252 atc gcc gag ttc gcc cgc atg ggc tgg gac ccg gca gtc gtg ccc gac  
 1253 1871  
 1254 Ile Ala Glu Phe Ala Arg Met Gly Trp Asp Pro Ala Val Val Pro Asp  
 1255 450 455 460 465  
 E--> 1257 ccg cag gac ccg gcc acc ttc gcc cgc tcg cac ctg gac tgg tcc gag  
 1258 1919  
 1259 Pro Gln Asp Pro Ala Thr Phe Ala Arg Ser His Leu Asp Trp Ser Glu  
 1260 470 475 480  
 E--> 1262 ccc gag cgg gaa ccg cac gcg ggc ctg ctc gcc ttc tac acc gac ctg  
 1263 1967  
 1264 Pro Glu Arg Glu Pro His Ala Gly Leu Leu Ala Phe Tyr Thr Asp Leu  
 1265 485 490 495  
 E--> 1267 atc gcg ctg cgg cgc gag ctg ccg gtc gat gcg ccg gcg cgc gag gtc  
 1268 2015



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Input Set : A:\Yamamtol.app  
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1269 Ile Ala Leu Arg Arg Glu Leu Pro Val Asp Ala Pro Ala Arg Glu Val  
1270 500 505 510  
**E--> 1272 gat gcc gac gag gcg cgc ggc gtc ttc gcg ttc agc cgc ggc ccg ctg**  
1273 2063  
1274 Asp Ala Asp Glu Ala Arg Gly Val Phe Ala Phe Ser Arg Gly Pro Leu  
1275 515 520 525  
**E--> 1277 cgg gtc acg gtc gcg ctg cgc ccc gga ccg gtc ggg gtg ccc gag cac**  
1278 2111  
1279 Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu His  
1280 530 535 540 545  
**E--> 1282 ggg ggc ctc gtg ctc gcc tac ggc gag gtg cgc gcc ggc gcc gca gga**  
1283 2159  
1284 Gly Gly Leu Val Leu Ala Tyr Gly Glu Val Arg Ala Gly Ala Ala Gly  
1285 550 555 560  
**E--> 1287 ctg cac ctc gac ggg ccg gga gcc gcg atc gtg cgc ctc gag**  
1288 2201  
1289 Leu His Leu Asp Gly Pro Gly Ala Ala Ile Val Arg Leu Glu  
1290 565 570 575  
**E--> 1292 tgacgcggct gggtacc**  
1293 2218  
1296 <210> SEQ ID NO: 33  
1297 <211> LENGTH: 25  
1298 <212> TYPE: DNA  
1299 <213> ORGANISM: Artificial Sequence  
1301 <220> FEATURE:  
1302 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
1304 <400> SEQUENCE: 33  
**E--> 1305 atgaaccgac gattcccggt ctggg**  
1306 25  
1308 <210> SEQ ID NO: 34  
1309 <211> LENGTH: 25  
1310 <212> TYPE: DNA  
1311 <213> ORGANISM: Artificial Sequence  
1313 <220> FEATURE:  
1314 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC  
1316 <400> SEQUENCE: 34  
**E--> 1317 tcactcgagg cgcacgatcg cggct**  
1318 25

*Patent*

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001  
TIME: 14:32:15

Input Set : A:\Yamamtol.app  
Output Set: N:\CRF3\01242001\I435770.raw

L:247 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7  
M:254 Repeated in SeqNo=7  
L:331 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:8  
L:535 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:17  
M:254 Repeated in SeqNo=17  
L:601 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:18  
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19  
M:254 Repeated in SeqNo=19  
L:922 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:20  
L:935 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:21  
L:948 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:22  
L:961 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:23  
L:974 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:24  
L:987 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:25  
L:1000 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:26  
L:1013 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:27  
L:1026 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:28  
L:1039 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:29  
L:1052 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:30  
L:1065 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31  
L:1065 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31  
L:1065 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31  
L:1065 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:31  
L:1085 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32  
differs:33  
L:1086 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:32  
M:254 Repeated in SeqNo=32  
L:1305 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:33  
L:1317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:34  
L:1330 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:35  
L:1343 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:36  
L:1356 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:37  
L:1369 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:38  
L:1382 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:39